

Attorney Docket No. 5470-130DV

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re: French et al.
Serial No.: 09/497,822
Filed: February 3, 2000

Confirmation No. 7943
Group Art Unit: 1646
Examiner: M. Pak

For: ANDROGEN RECEPTOR PROTEINS, RECOMBINANT DNA MOLECULES
CODING FOR SUCH, AND USE OF SUCH COMPOSITIONS

Date: November 26, 2002

Commissioner for Patents
Washington, DC 20231

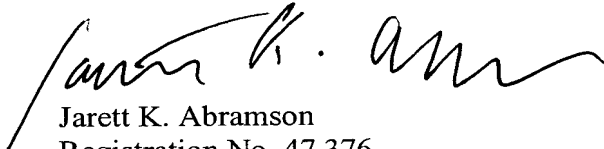
**STATEMENT IN SUPPORT OF FILING A
SEQUENCE LISTING UNDER 37 CFR § 1.821(f)**

RECEIVED
DEC 05 2002
TECH CENTER 1600/2900

Sir:

I hereby state that the content of the paper and computer readable copies of the Sequence listing are the same. I also hereby state as required by 37 CFR § 1.821(h) that the computer readable copy submitted concurrently herewith contains no new matter, nor does it go beyond the disclosure of the application as filed.

Respectfully submitted,


Jarett K. Abramson
Registration No. 47,376

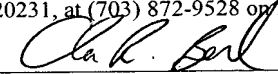


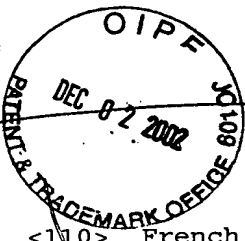
20792

PATENT TRADEMARK OFFICE

CERTIFICATE OF FACSIMILE TRANSMISSION

I hereby certify that this correspondence is being sent by facsimile transmission to Commissioner for Patents, Washington, DC 20231, at (703) 872-9528 on November 26, 2002.


Clara R. Beard



SEQUENCE LISTING

<110> French, Frank
Wilson, Elizabeth
Joseph, David
Lubahn, Dennis

<120> ANDROGEN RECEPTOR PROTEINS RECOMBINANT DNA MOLECULES AND CODING
FOR SUCH AND USE OF SUCH COMPOSITIONS

<130> 5470-130DV

<140> US 09/497,822

<141> 2000-02-03

<160> 26

<170> PatentIn version 3.1

<210> 1

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 1

acctgtgagg gctgtaaggt cttcttcaaa ag

32

<210> 2

<211> 32

<212> DNA

<213> Homo sapiens

<400> 2

acatgtggaa gctgcaaggt cttcttcaaa ag

32

<210> 3

<211> 32

<212> DNA

<213> Homo sapiens

<400> 3

acctgtggga gctgtaaggt cttctttaag ag

32

<210> 4

<211> 32

<212> DNA

<213> Homo sapiens

<400> 4

acctgtggca gctgcaaagt tttcttcaaa ag

32

<210> 5

<211> 32

<212> DNA

RECEIVED
DEC 05 2002
TECH CENTER 1600/2900

Sub
EI
D

<213> Homo sapiens

<400> 5
acttgtggaa gctgtaaagt tttcttcaaa ag

32

<210> 6
<211> 32
<212> DNA
<213> Homo sapiens

<400> 6
tcctgtgagg gctgtaaggc cttcttcaag ag

32

<210> 7
<211> 32
<212> DNA
<213> Homo sapiens

<400> 7
acgtgtgaag gctgcaaggg tttctttaga ag

32

<210> 8
<211> 32
<212> DNA
<213> Homo sapiens

<400> 8
gcctgtgagg gctgcaaggg cttcttccgc cg

32

<210> 9
<211> 66
<212> PRT
<213> Homo sapiens

<400> 9

Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu
1 5 10 15

Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys
20 25 30

Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe
35 40 45

Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala
50 55 60

Gly Met
65

<210> 10

<211> 66
<212> PRT
<213> Homo sapiens

<400> 10

Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Val Leu
1 5 10 15

Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Met Glu Gly Gln
20 25 30

His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile Val Asp Lys Ile
35 40 45

Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu Arg Lys Cys Cys Gln Ala
50 55 60

Gly Met
65

<210> 11
<211> 66
<212> PRT
<213> Homo sapiens

<400> 11

Cys Leu Val Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Val Val
1 5 10 15

Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Val Glu Gly Gln
20 25 30

His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile Ile Asp Lys Ile
35 40 45

Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu Gln Lys Cys Leu Gln Ala
50 55 60

Gly Met
65

<210> 12
<211> 66
<212> PRT
<213> Homo sapiens

<400> 12

Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His Tyr Gly Val Leu

1 5 10 15

Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Val Glu Gly Gln
 20 25 30

His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile Ile Asp Lys Ile
 35 40 45

Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys Cys Leu Gln Ala
 50 55 60

Gly Met
 65

<210> 13
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 13

Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp
 1 5 10 15

Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His
 20 25 30

Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn
 35 40 45

Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val
 50 55 60

Gly Met
 65

<210> 14
 <211> 66
 <212> PRT
 <213> Gallus gallus

<400> 14

Cys Gly Val Cys Gly Asp Arg Ala Thr Gly Phe His Phe Asn Ala Met
 1 5 10 15

Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Met Lys Arg Lys
 20 25 30

Ala Met Phe Thr Cys Pro Phe Asn Gly Asp Cys Lys Ile Thr Lys Asp
 35 40 45

Asn Arg Arg His Cys Gln Ala Cys Arg Leu Lys Arg Cys Val Asp Ile
 50 55 60

Gly Met
 65

<210> 15
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 15

Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His Tyr Arg Cys Ile
 1 5 10 15

Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Gln Lys Asn
 20 25 30

Leu His Pro Ser Tyr Ser Cys Lys Tyr Glu Gly Lys Cys Val Ile Asp
 35 40 45

Lys Val Thr Arg Asn Gln Cys Gln Glu Cys Arg Phe Lys Lys Cys Ile
 50 55 60

Tyr Val Gly Met
 65

<210> 16
 <211> 68
 <212> PRT
 <213> Avian erythroblastosis virus

<400> 16

Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His Tyr Arg Cys Ile
 1 5 10 15

Thr Cys Glu Gly Cys Lys Ser Phe Phe Arg Arg Thr Ile Gln Lys Asn
 20 25 30

Leu His Pro Thr Thr Ser Cys Thr Tyr Asp Gly Cys Cys Val Ile Asp
 35 40 45

Lys Ile Thr Arg Asn Gln Cys Gln Leu Cys Arg Phe Lys Lys Cys Ile
 50 55 60

Ser Val Gly Met
65

<210> 17
<211> 66
<212> PRT
<213> Homo sapiens

<400> 17

Cys Phe Val Cys Gln Asp Lys Ser Ser Gly Tyr His Tyr Gly Val Ser
1 5 10 15

Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Ile Gln Lys Asn
20 25 30

Met Val Tyr Thr Cys His Arg Asp Lys Asn Cys Ile Ile Asn Lys Val
35 40 45

Thr Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Lys Cys Phe Glu Val
50 55 60

Gly Met
65

<210> 18
<211> 5082
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (360)..(360)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (365)..(365)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (376)..(376)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (385)..(385)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (399)..(399)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (407)..(407)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (417)..(417)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (422)..(422)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (435)..(435)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (439)..(439)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (441)..(441)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (598)..(598)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (689)..(689)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (714)..(715)
<223> "n" denotes any nucleotide

<220>

<221> misc_feature
<222> (844)..(844)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (870)..(870)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (918)..(918)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (932)..(932)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1195)..(1195)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1198)..(1198)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1202)..(1202)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1248)..(1248)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (1322)..(1322)
<223> "n" denotes any nucleotide

<220>
<221> CDS
<222> (1864)..(4632)
<223>

<400> 18
gagctctgga caaaattgag cgcctatgtg tacatggcaa gtgttttttag tgtttgtgtg

60

tttacctgct	tgtctgggtg	atthttgcctt	tgagagtctg	gatgagaaat	gcatgggttaa	120
aggcaattcc	agacaggaag	aaaggcagag	aagagggtag	aatgacctc	tgattcttgg	180
ggctgagggt	tcctagagca	aatggcacaa	tgccacgagg	ccgatctat	ccctatgacg	240
gaactctaag	gtttcagcat	cagctatctg	ctggcttgg	cactggcttg	cctcctcagt	300
ttgtaggaga	ctctcccact	ctcccatctg	cgcgctctta	tcagtctctga	aaagaaccn	360
tggcnagcca	ggagcnaggt	attcntatcg	tccttttct	cctcctngcc	tcacctngtt	420
gntttttaga	ttggncctng	naaccaaatt	tgtatgctgg	cctccaggaa	atctggagcc	480
tggcgcttaa	accttggttt	aggaaaagcag	gagctattca	ggaagcaggg	tcctccaggg	540
ctagagctag	cctctcctgc	cctcgccac	gtgcgccagc	acttgtttct	ccaaagcnac	600
taggcaggcg	ttagcgcgcg	gtgaggggag	gggagaaaag	gaaaggggag	gggagggaaa	660
aggaggtggg	aaggcaagga	ggccggccng	gtgggggagg	gacccgactc	gcannaactg	720
ttgcatttgc	tctccacctc	ccagcgcccc	ctccgagatc	ccggggagcc	agcttgctgg	780
gagagcgga	acggtccgga	gcaagcccag	aggcagagga	ggcgacagag	ggaaaaaggg	840
ccnagctag	ccgctccagt	gctgtacagn	agccgaagga	cgcaccacgc	cagccccagc	900
ccggctccag	cgacagcnaa	cgctcttgc	angcgttcga	agccgcccgc	cggagctgcc	960
ctttcctctt	cgggtgaagt	tttaaaagct	gctaaagact	cggaggaagc	aaggaaagtg	1020
cctggtagga	ctgacggctg	cctttgtcct	cctcctctcc	accccgctc	ccccaccct	1080
gccttcccc	cctcccccg	cttctctccc	gcagctgcct	cagtccgcta	ctctcagcca	1140
acccccctca	ccacccttct	ccccaccgc	cccccgccc	ccgtcggccc	agcgnatgna	1200
gnccgagttt	gcagagaggt	aactcccttt	ggctgcgagc	gggcgagnct	agctgcacat	1260
tgcaaaag	gctcttagga	gcaggcgact	ggggagcggc	ttcagcactg	cagccacgac	1320
cngcctgggt	aggctgcacg	cggagagaac	cctctgtttt	ccccactct	ctctccacct	1380
cctcctgcct	ccccacccc	gagtgcggag	ccagagatca	aaagatgaaa	aggcagtcag	1440
gtcttcagta	gcaaaaaaac	aaaacaaaca	aaaacaaaaa	agccgaaata	aaagaaaaag	1500
ataataactc	agttcttatt	tgacacctact	tcagtggaca	ctgaatttgg	aagggtggag	1560
atthttgttt	tttcttttaa	gatctgggca	tcttttgaat	ctacccttca	agtattaaga	1620
gacagactgt	gagcctagca	gggcagatct	tgtccaccgt	gtgtcttctt	ctgcacgaga	1680
ctttgaggct	gtcagagcgc	tttttgctg	gttgctccc	caagtttct	tctctggagc	1740
ttcccgagg	tgggcagcta	gctgcagcga	ctaccgcac	atcacagcct	gttgaaactct	1800
tctgagcaag	agaaggggag	gcggggtaag	ggaagtaggt	ggaagattca	gccaagctca	1860

agg atg gaa gtg cag tta ggg ctg gga agg gtc tac cct cgg ccg ccg	1908
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro	
1 5 10 15	
tcc aag acc tac cga gga gct ttc cag aat ctg ttc cag agc gtg cgc	1956
Ser Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg	
20 25 30	
gaa gtg atc cag aac ccg ggc ccc agg cac cca gag gcc gcg agc gca	2004
Glu Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala	
35 40 45	
gca cct ccc ggc gcc agt ttg ctg ctg ctg cag cag cag cag cag cag	2052
Ala Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln	
50 55 60	
cag cag cag cag cag cag cag cag cag cag cag cag cag cag cag	2100
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
65 70 75	
cag cag caa gag act agc ccc agg cag cag cag cag cag cag ggt gag	2148
Gln Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gly Glu	
80 85 90 95	
gat ggt tct ccc caa gcc cat cgt aga ggc ccc aca ggc tac ctg gtc	2196
Asp Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val	
100 105 110	
ctg gat gag gaa cag caa cct tca cag ccg cag tcg gcc ctg gag tgc	2244
Leu Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys	
115 120 125	
cac ccc gag aga ggt tgc gtc cca gag cct gga gcc gcc gtg gcc gcc	2292
His Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala	
130 135 140	
agc aag ggg ctg ccg cag cag ctg cca gca cct ccg gac gag gat gac	2340
Ser Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp	
145 150 155	
tca gct gcc cca tcc acg ttg tcc ctg ctg ggc ccc act ttc ccc ggc	2388
Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly	
160 165 170 175	
tta agc agc tgc tcc gct gac ctt aaa gac atc ctg agc gag gcc agc	2436
Leu Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser	
180 185 190	
acc atg caa ctc ctt cag caa cag cag cag gaa gca gta tcc gaa ggc	2484
Thr Met Gln Leu Leu Gln Gln Gln Gln Glu Ala Val Ser Glu Gly	
195 200 205	
agc agc agc ggg aga gcg agg gag gcc tcg ggg gct ccc act tcc tcc	2532
Ser Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser	
210 215 220	
aag gac aat tac tta ggg ggc act tcg acc att tct gac aac gcc aag	2580
Lys Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys	
225 230 235	
gag ttg tgt aag gca gtg tcg gtg tcc atg ggc ctg ggt gtg gag gcg	2628

Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala	
240 245 250 255	
ttg gag cat ctg agt cca ggg gaa cag ctt cgg ggg gat tgc atg tac	2676
Leu Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr	
260 265 270	
gcc cca ctt ttg gga gtt cca ccc gct gtg cgt ccc act cct tgt gcc	2724
Ala Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala	
275 280 285	
cca ttg gcc gaa tgc aaa ggt tct ctg cta gac gac agc gca ggc aag	2772
Pro Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys	
290 295 300	
agc act gaa gat act gct gag tat tcc cct ttc aag gga ggt tac acc	2820
Ser Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr	
305 310 315	
aaa ggg cta gaa ggc gag agc cta ggc tgc tct ggc agc gct gca gca	2868
Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala	
320 325 330 335	
ggg agc tcc ggg aca ctt gaa ctg ccg tct acc ctg tct ctc tac aag	2916
Gly Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys	
340 345 350	
tcc gga gca ctg gac gag gca gct gcg tac cag agt cgc gac tac tac	2964
Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr	
355 360 365	
aac ttt cca ctg gct ctg gcc gga ccg ccg ccc cct ccg ccg cct ccc	3012
Asn Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro Pro	
370 375 380	
cat ccc cac gct cgc atc aag ctg gag aac ccg ctg gac tac ggc agc	3060
His Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser	
385 390 395	
gcc tgg gcg gct gcg gcg gcg cag tgc cgc tat ggg gac ctg gcg agc	3108
Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser	
400 405 410 415	
ctg cat ggc gcg ggt gca gcg gga ccc ggt tct ggg tca ccc tca gcc	3156
Leu His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala	
420 425 430	
gcc gct tcc tca tcc tgg cac act ctc ttc aca gcc gaa gaa ggc cag	3204
Ala Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln	
435 440 445	
ttg tat gga ccg tgt ggt ggt ggt ggg ggt ggt ggc ggc ggc ggc ggc	3252
Leu Tyr Gly Pro Cys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly	
450 455 460	
ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc gag gcg gga	3300
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly	
465 470 475	
gct gta gcc ccc tac ggc tac act cgg ccc cct cag ggg ctg gcg ggc	3348
Ala Val Ala Pro Tyr Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly	

480	485	490	495	
cag gaa agc gac ttc acc gca cct gat gtg tgg tac cct ggc ggc atg Gln Glu Ser Asp Phe Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met 500 505 510				3396
gtg agc aga gtg ccc tat ccc agt ccc act tgt gtc aaa agc gaa atg Val Ser Arg Val Pro Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met 515 520 525				3444
ggc ccc tgg atg gat agc tac tcc gga cct tac ggg gac atg cgt ttg Gly Pro Trp Met Asp Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu 530 535 540				3492
gag act gcc agg gac cat gtt ttg ccc att gac tat tac ttt cca ccc Glu Thr Ala Arg Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro 545 550 555				3540
cag aag acc tgc ctg atc tgt gga gat gaa gct tct ggg tgt cac tat Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr 560 565 570 575				3588
gga gct ctc aca tgt gga agc tgc aag gtc ttc ttc aaa aga gcc gct Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala 580 585 590				3636
gaa ggg aaa cag aag tac ctg tgc gcc agc aga aat gat tgc act att Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile 595 600 605				3684
gat aaa ttc cga agg aaa aat tgt cca tct tgt cgt ctt cgg aaa tgt Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys 610 615 620				3732
tat gaa gca ggg atg act ctg gga gcc cgg aag ctg aag aaa ctt ggt Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly 625 630 635				3780
aat ctg aaa cta cag gag gaa gga gag gct tcc agc acc acc agc ccc Asn Leu Lys Leu Gln Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro 640 645 650 655				3828
act gag gag aca acc cag aag ctg aca gtg tca cac att gaa ggc tat Thr Glu Glu Thr Thr Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr 660 665 670				3876
gaa tgt cag ccc atc ttt ctg aat gtc ctg gaa gcc att gag cca ggt Glu Cys Gln Pro Ile Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly 675 680 685				3924
gta gtg tgt gct gga cac gac aac aac cag ccc gac tcc ttt gca gcc Val Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala 690 695 700				3972
ttg ctc tct agc ctc aat gaa ctg gga gag aga cag ctt gta cac gtg Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val 705 710 715				4020
gtc aag tgg gcc aag gcc ttg cct ggc ttc cgc aac tta cac gtg gac Val Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp 720 725 730 735				4068

DI
Cont

gac cag atg gct gtc att cag tac tcc tgg atg ggg ctc atg gtg ttt Asp Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe 740 745 750	4116
gcc atg ggc tgg cga tcc ttc acc aat gtc aac tcc agg atg ctc tac Ala Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr 755 760 765	4164
ttc gcc cct gat ctg gtt ttc aat gag tac cgc atg cac aag tcc cgg Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg 770 775 780	4212
atg tac agc cag tgt gtc cga atg agg cac ctc tct caa gag ttt gga Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly 785 790 795	4260
tgg ctc caa atc acc ccc cag gaa ttc ctg tgc atg aaa gca ctg cta Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu 800 805 810 815	4308
ctc ttc agc att att cca gtg gat ggg ctg aaa aat caa aaa ttc ttt Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe 820 825 830	4356
gat gaa ctt cga atg aac tac atc aag gaa ctc gat cgt atc att gca Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala 835 840 845	4404
tgc aaa aga aaa aat ccc aca tcc tgc tca aga cgc ttc tac cag ctc Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu 850 855 860	4452
acc aag ctc ctg gac tcc gtg cag cct att gcg aga gag ctg cat cag Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln 865 870 875	4500
ttc act ttt gac ctg cta atc aag tca cac atg gtg agc gtg gac ttt Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe 880 885 890 895	4548
ccg gaa atg atg gca gag atc atc tct gtg caa gtg ccc aag atc ctt Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu 900 905 910	4596
tct ggg aaa gtc aag ccc atc tat ttc cac acc cag tgaagcattg Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln 915 920	4642
gaaaccctat ttccccaccc cagctcatgc cccctttcag atgtcttctg cctgttataa	4702
ctctgcacta ctccctctgca gtgccttggg gaatttcctc tattgatgta cagtctgtca	4762
tgaacatggt cctgaattct atttgctggg cttttttttt ctctttctct cctttctttt	4822
tcttttcccc tccctatcta accctcccat ggcaccttca gactttgctt cccattgtgg	4882
ctcctatctg tgttttgaat ggtgttgtat gccttttaa ctgtgatgat cctcatatgg	4942
cccagtgtca agttgtgctt gtttacagca ctactctgtg ccagccacac aaacgtttac	5002

DI
Cont

ttatcttatg ccacgggaag tttagagagc taagattatc tggggaaatc aaaacaaaaa 5062
acaagcaaac aaaaaaaaaa 5082

<210> 19
<211> 923
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (360)..(360)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (365)..(365)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (376)..(376)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (385)..(385)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (399)..(399)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (407)..(407)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (417)..(417)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (422)..(422)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (435)..(435)
<223> "n" denotes any nucleotide

<220>
<221> misc_feature
<222> (439)..(439)
<223> "n" denotes any nucleotide

<220>

D!
Cont.

<221> misc_feature
 <222> (441)..(441)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (598)..(598)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (689)..(689)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (714)..(715)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (844)..(844)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (870)..(870)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (918)..(918)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (932)..(932)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (1195)..(1195)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (1198)..(1198)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (1202)..(1202)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature
 <222> (1248)..(1248)
 <223> "n" denotes any nucleotide

 <220>
 <221> misc_feature

D1
 cont.

<222> (1322)..(1322)
 <223> "n" denotes any nucleotide

<400> 19

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
 1 5 10 15

Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
 20 25 30

Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
 35 40 45

Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
 50 55 60

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80

Gln Gln Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gly Glu Asp
 85 90 95

Gly Ser Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu
 100 105 110

Asp Glu Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His
 115 120 125

Pro Glu Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser
 130 135 140

Lys Gly Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser
 145 150 155 160

Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu
 165 170 175

Ser Ser Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr
 180 185 190

Met Gln Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser
 195 200 205

Ser Ser Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys
 210 215 220

Asp Asn Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu
225 230 235 240

Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu
245 250 255

Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala
260 265 270

Pro Leu Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro
275 280 285

Leu Ala Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser
290 295 300

Thr Glu Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys
305 310 315 320

Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly
325 330 335

Ser Ser Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser
340 345 350

Gly Ala Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn
355 360 365

Phe Pro Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro His
370 375 380

Pro His Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala
385 390 395 400

Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu
405 410 415

His Gly Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala
420 425 430

Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu
435 440 445

Tyr Gly Pro Cys Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
450 455 460

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala

DI
Cont

465		470		475		480									
Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln
				485					490					495	
Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val
			500					505					510		
Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly
		515					520					525			
Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu
	530					535					540				
Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln
545					550					555					560
Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly
				565					570					575	
Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu
			580					585					590		
Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp
		595					600					605			
Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr
	610					615					620				
Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn
625					630					635					640
Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr
				645					650					655	
Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu
			660					665					670		
Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val
		675					680					685			
Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu
	690					695					700				
Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	Val
705				710						715					720

D1 Cont

Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp
725 730 735

Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala
740 745 750

Met Gly Trp Arg Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe
755 760 765

Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met
770 775 780

Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp
785 790 795 800

Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu
805 810 815

Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp
820 825 830

Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys
835 840 845

Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr
850 855 860

Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe
865 870 875 880

Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro
885 890 895

Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser
900 905 910

Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln
915 920

<210> 20
<211> 4289
<212> DNA
<213> Rattus rattus

<220>
<221> CDS

<222> (1123)..(3828)
<223>

<400> 20
aattcgggaa ggatcgagca aaccaggaaa gtaaggatgg agatcctagg agagtgtcca 60
tgctcggaaa ggagcccacc aaagatgaac tgttgcatTTt gctttccacc tcccagcgcc 120
ccctcggaga tccctaggag ccagcctgct gggagaacca gaggggtccgg agcaaacctg 180
gaggctgaga gggcatcaga ggggaaaaga ctgagttagc cactccagtg ccatacagaa 240
gcttaaggga cataccacgc cagccccagc ccagcgacag ccaacgcctg ttgcagagcg 300
gcggttctga agccgcccgc cagaagctgc cctttcctct tcggtgaagt ttctaaaagc 360
tgcgggagac tcggaggaag cgaagaaagt gtccggtagg actacgactg cctttgtcct 420
cctccctcct acccctaccc ctctgggtc cctctccct gagcggacta ggcaggcttc 480
ctggccagcc ctctccccta caccaccagc tctgccagcc agtttgcaca gaggtaactc 540
cctttggctg aaagcagacg agcttggtgc ccattggaag ggaggctttt gggagcccag 600
agactgagga gcaacagcac gctggagagt cctgattcc aggttctccc cctgcacct 660
cctactgcc gccccctacc ctgtgtgtgc agctagaatt gaaaagatga aaagacagtt 720
ggggcttcag tagtcgaaag caaaacaaaa gcaaaaagaa aacaaaaaga aaatagccca 780
gttcttattt gcacctgctt cagtggacat tgactttgga aggagagaa ttttccttcc 840
ccccagtcaa gctttgagca tcttttaatc tgttcttcaa gtatttaggg acaaactgtg 900
aaactagcag ggcagatcct gtctagcgcg tgccttcctt tacaggagac tttgaggcta 960
tctgggcgct cccccccctc cctgcaagtt ttcttcctg gagcttcccg cagggtgggca 1020
gctagctgca gatactacat catcagtcag tagaactctt cagagcaaga gacgaggagg 1080
caggataagg gaattcgggtg gaagctagag acaagctaaa gg atg gag gtg cag 1134
Met Glu Val Gln
1
tta ggg ctg gga agg gtc tac cca cgg ccc ccg tcc aag acc tat cga 1182
Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser Lys Thr Tyr Arg
5 10 15 20
gga gcg ttc cag aat ctg ttc cag agc gtg cgc gaa gcg atc cag aac 1230
Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu Ala Ile Gln Asn
25 30 35
ccg ggc ccc agg cac cct gag gcc gct agc ata gca cct ccc ggt gcc 1278
Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile Ala Pro Pro Gly Ala
40 45 50
tgt tta cag cag cgg cag gag act agc ccc cgg cgg cgg cgg cgg cag 1326
Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg Arg Arg Arg Gln
55 60 65

cag cac cct gag gat ggc tct cct caa gcc cac atc aga ggc acc aca Gln His Pro Glu Asp Gly Ser Pro Gln Ala His Ile Arg Gly Thr Thr 70 75 80	1374
ggc tac ctg gcc ctg gag gag gaa cag cag cct tca cag cag cag tca Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser Gln Gln Gln Ser 85 90 95 100	1422
gcc tcc gag ggc cac cct gag agc ggc tgc ctc ccg gag cct gga gct Ala Ser Glu Gly His Pro Glu Ser Gly Cys Leu Pro Glu Pro Gly Ala 105 110 115	1470
gcc acg gct cct ggc aag ggg ctg ccg cag cag cca cca gct cct cca Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro Pro Ala Pro Pro 120 125 130	1518
gat cag gat gac tca gct gcc cca tcc acg ttg tcc cta ctg ggc ccc Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro 135 140 145	1566
act ttc cca ggc tta agc agc tgc tcc gca gac att aaa gac atc ctg Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile Lys Asp Ile Leu 150 155 160	1614
agc gag gcc ggc acc atg caa ctt ctt cag cag cag cag caa cag caa Ser Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln Gln Gln Gln 165 170 175 180	1662
cag cag cag cag cag cag cag cag cag cag cag cag cag cag cag gag Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu 185 190 195	1710
gta ata tcc gaa ggc agc agc agc gtg aga gca agg gag gcc act ggg Val Ile Ser Glu Gly Ser Ser Ser Val Arg Ala Arg Glu Ala Thr Gly 200 205 210	1758
gct ccc tct tcc tcc aag gat agt tac cta ggg ggc aat tcg acc ata Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr Ile 215 220 225	1806
tct gac agt gcc aag gag ttg tgt aaa gca gtg tct gtg tcc atg ggg Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly 230 235 240	1854
ttg ggt gtg gaa gca ctg gaa cat ctg agt cca ggg gag cag ctt cgg Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu Arg 245 250 255 260	1902
ggc gac tgc atg tac gcg tcg ctc ctg gga ggt cca ccc gcc gtg cgt Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val Arg 265 270 275	1950
ccc act cct tgt gcg cct ctg gcc gaa tgc aaa ggt ctt tcc ctg gac Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly Leu Ser Leu Asp 280 285 290	1998
gaa ggc ccg ggc aaa ggc act gaa gag act gct gag tat tcc tct ttc Glu Gly Pro Gly Lys Gly Thr Glu Glu Thr Ala Glu Tyr Ser Ser Phe 295 300 305	2046
aag gga ggt tac gcc aaa ggg ttg gaa ggt gag agt ctg ggc tgc tct	2094

D1
Cont

Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser		
310						315					320						
ggc	agc	agt	gaa	gca	ggt	agc	tct	ggg	aca	ctt	gag	atc	ccg	tcc	tca	2142	
Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser	Ser		
325					330					335					340		
ctg	tct	ctg	tat	aag	tct	gga	gca	gta	gac	gag	gca	gca	gca	tac	cag	2190	
Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Val	Asp	Glu	Ala	Ala	Ala	Tyr	Gln		
				345					350					355			
aat	cgc	gac	tac	tac	aac	ttt	ccg	ctc	gct	ctg	tcc	ggg	ccg	ccg	cac	2238	
Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro	His		
			360					365					370				
ccc	ccg	ccc	cct	acc	cat	cca	cac	gcc	cgc	atc	aag	ctg	gag	aac	ccg	2286	
Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	Pro		
		375					380					385					
tcg	gac	tac	ggc	agc	gcc	tgg	gct	gcg	gcg	gca	gcg	caa	tgc	cgc	tat	2334	
Ser	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr		
	390					395					400						
ggg	gac	ttg	gct	agc	cta	cat	gga	ggg	agt	gta	gcc	gga	ccc	agc	act	2382	
Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser	Thr		
405					410					415					420		
gga	tcg	ccc	cca	gcc	acc	gcc	tct	tct	tcc	tgg	cat	act	ctc	ttc	aca	2430	
Gly	Ser	Pro	Pro	Ala	Thr	Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr		
				425					430					435			
gct	gaa	gaa	ggc	caa	tta	tat	ggg	cca	gga	ggc	ggg	ggc	ggc	agc	agt	2478	
Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser	Ser		
			440					445					450				
agc	cca	agc	gat	gct	ggg	cct	gta	gcc	ccc	tat	ggc	tac	act	cgg	ccc	2526	
Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro		
			455				460					465					
cct	cag	ggg	ctg	gca	agc	cag	gag	ggt	gac	ttc	tct	gcc	tct	gaa	gtg	2574	
Pro	Gln	Gly	Leu	Ala	Ser	Gln	Glu	Gly	Asp	Phe	Ser	Ala	Ser	Glu	Val		
	470					475					480						
tgg	tat	cct	ggt	gga	gtt	gtg	aac	aga	gtc	ccc	tat	ccc	agt	ccc	agt	2622	
Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Ser		
485					490					495					500		
tgt	gtt	aaa	agt	gaa	atg	gga	cct	tgg	atg	gag	aac	tac	tcc	gga	cct	2670	
Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly	Pro		
				505					510					515			
tat	ggg	gac	atg	cgt	ttg	gac	agt	acc	agg	gac	cac	gtt	tta	ccc	atc	2718	
Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro	Ile		
				520				525					530				
gac	tat	tac	ttc	cca	ccc	cag	aag	acc	tgc	ctg	atc	tgt	gga	gat	gaa	2766	
Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu		
			535				540					545					
gct	tct	ggt	tgt	cac	tac	gga	gct	ctc	act	tgt	ggc	agc	tgc	aag	gtc	2814	
Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val		

Cont

550	555	560	
ttc ttc aaa aga gct gcg gaa ggg aaa cag aag tat cta tgt gcc agc			2862
Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser			
565	570	575	580
aga aat gat tgc acc att gat aaa ttt cgg agg aaa aat tgt cca tcg			2910
Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser			
	585	590	595
tgt cgt ctc cgg aaa tgt tat gaa gca ggg atg act ctg gga gct cgt			2958
Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg			
	600	605	610
aag ctg aag aaa ctt gga aat ctc aaa cta cag gaa gaa gga gaa aac			3006
Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu Asn			
	615	620	625
tcc agt gct ggt agc ccc act gag gac cca tcc cag aag atg act gta			3054
Ser Ser Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr Val			
	630	635	640
tca cac att gaa ggc tat gaa tgt caa cct atc ttt ctt aat gtc ctg			3102
Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val Leu			
	645	650	655
gaa gcc att gag cca gga gtg gtg tgt gcc gga cat gac aac aac cag			3150
Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn Gln			
	665	670	675
cct gat tcc ttt gct gcc ttg tta tct agt ctc aac gag ctt ggc gag			3198
Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu			
	680	685	690
aga cag ctt gta cat gtg gtc aag tgg gcc aag gcc ttg cct ggc ttc			3246
Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly Phe			
	695	700	705
cgc aac ttg cat gtg gat gac cag atg gca gtc att cag tat tcc tgg			3294
Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser Trp			
	710	715	720
atg gga ctg atg gta ttt gcc atg ggt tgg cgg tcc ttc act aat gtc			3342
Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn Val			
	725	730	735
aac tct agg atg ctc tac ttt gca cct gac ctg gtt ttc aat gag tat			3390
Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr			
	745	750	755
cgc atg cac aag tct cga atg tac agc cag tgc gtg agg atg agg cac			3438
Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg His			
	760	765	770
ctt tct caa gag ttt gga tgg ctc cag ata acc ccc cag gaa ttc ctg			3486
Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu			
	775	780	785
tgc atg aaa gca ctg cta ctc ttc agc att att cca gtg gat ggg ctg			3534
Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly Leu			
	790	795	800

DI
Cont

aaa aat caa aaa ttc ttt gat gaa ctt cga atg aac tac atc aag gaa	3582
Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu	
805 810 815 820	
ctt gat cgc atc att gca tgc aaa aga aaa aat ccc aca tcc tgc tca	3630
Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser	
825 830 835	
agg cgc ttc tac cag ctc acc aag ctc ctg gat tct gtg cag cct att	3678
Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile	
840 845 850	
gca aga gag ctg cat caa ttc act ttt gac ctg cta atc aag tcc cat	3726
Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His	
855 860 865	
atg gtg agc gtg gac ttt cct gaa atg atg gca gag atc atc tct gtg	3774
Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val	
870 875 880	
caa gtg ccc aag atc ctt tct ggg aaa gtc aag ccc atc tat ttc cac	3822
Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His	
885 890 895 900	
aca cag tgaagatttg gaacctaata cccaaaccca cctgttcctt tttcagatgt	3878
Thr Gln	
cttctgacctg ttatataact ctgcactact tctctggcat gggccttggg ggaaattcct	3938
ctactgatgt acagtctgtc atgaacatgt tccccagtt ctatttcctg ggcttttctt	3998
tctttctttt tctttctctc tgcctctttt accctcccat ggcacatttt gaatccgctg	4058
cgtgttggtg ctctgacctg tgttttgagt tttgttgat ttcttcaagt ctgtgatgat	4118
cttcttggtg cccagtgtca actgtgcttg tttatagcac tgtgctgtgt gccaaccaag	4178
caaatgttta ctacattat gccatggcaa gtttagagag ctataagtat cttgggaaga	4238
aacaaacaga gagagtaaaa aaaccaaaaa aaaaaaaaaa aaaccgaatt c	4289

<210> 21
 <211> 902
 <212> PRT
 <213> Rattus rattus

<400> 21

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1 5 10 15

Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
20 25 30

Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile Ala
35 40 45

Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
50 55 60

Arg Arg Arg Gln Gln His Pro Glu Asp Gly Ser Pro Gln Ala His Ile
65 70 75 80

Arg Gly Thr Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
85 90 95

Gln Gln Gln Ser Ala Ser Glu Gly His Pro Glu Ser Gly Cys Leu Pro
100 105 110

Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
115 120 125

Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
130 135 140

Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145 150 155 160

Lys Asp Ile Leu Ser Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
165 170 175

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
180 185 190

Gln Gln Gln Glu Val Ile Ser Glu Gly Ser Ser Ser Val Arg Ala Arg
195 200 205

Glu Ala Thr Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly
210 215 220

Asn Ser Thr Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser
225 230 235 240

Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly
245 250 255

Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro
260 265 270

Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly
275 280 285

Leu Ser Leu Asp Glu Gly Pro Gly Lys Gly Thr Glu Glu Thr Ala Glu
290 295 300

Tyr Ser Ser Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser
305 310 315 320

Leu Gly Cys Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu
325 330 335

Ile Pro Ser Ser Leu Ser Leu Tyr Lys Ser Gly Ala Val Asp Glu Ala
340 345 350

Ala Ala Tyr Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser
355 360 365

Gly Pro Pro His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys
370 375 380

Leu Glu Asn Pro Ser Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala
385 390 395 400

Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Gly Ser Val Ala
405 410 415

Gly Pro Ser Thr Gly Ser Pro Pro Ala Thr Ala Ser Ser Ser Trp His
420 425 430

Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly
435 440 445

Gly Gly Ser Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly
450 455 460

Tyr Thr Arg Pro Pro Gln Gly Leu Ala Ser Gln Glu Gly Asp Phe Ser
465 470 475 480

Ala Ser Glu Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr
485 490 495

Pro Ser Pro Ser Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn
500 505 510

Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His
515 520 525

Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile
530 535 540

Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly
545 550 555 560

Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr
565 570 575

Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys
580 585 590

Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr
595 600 605

Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu
610 615 620

Glu Gly Glu Asn Ser Ser Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln
625 630 635 640

Lys Met Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe
645 650 655

Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His
660 665 670

Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn
675 680 685

Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala
690 695 700

Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile
705 710 715 720

Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser
725 730 735

Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val
740 745 750

Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val
755 760 765

Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro

770

775

780

Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro
785 790 795 800

Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn
805 810 815

Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro
820 825 830

Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser
835 840 845

Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu
850 855 860

Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu
865 870 875 880

Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro
885 890 895

Ile Tyr Phe His Thr Gln
900

<210> 22
<211> 12
<212> DNA
<213> Artificial sequence

<220>
<223> Hypothetical oligonucleotide

<400> 22
gctgggttgta ag

12

<210> 23
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Hypothetical peptide

<400> 23

Ala Gly Cys Lys
1

<210> 24
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide probe A

<400> 24
cttttgaaga agaccttaca gccctcacag gt

32

<210> 25
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide probe B

<400> 25
ggaccatggtt ttgcccatgg actattactt tccacccc

38

<210> 26
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic peptide

<400> 26

Asp His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr
1 5 10 15



TGCGTGAGGATGAGGCACCTTTCTCAAGAGTTTGGATGGCTCCAGATAACCCCCCAGGAA 3480
CysValArgMetArgHisLeuSerGlnGluPheGlyTrpLeuGlnIleThrProGlnGlu

TTCCTGTGCATGAAAGCACTGCTACTCTTCAGCATTATTCCAGTGGATGGGCTGAAAAAT 3540
PheLeuCysMetLysAlaLeuLeuLeuPheSerIleIleProValAspGlyLeuLysAsn

CAAAAATTCTTTGATGAACTTCGAATGAACTACATCAAGGAACTTGATCGCATCATTGCA 3600
GlnLysPhePheAspGluLeuArgMetAsnTyrIleLysGluLeuAspArgIleIleAla

TGCAAAAGAAAAAATCCCACATCCTGCTCAAGGCGCTTCTACCAGCTCACCAAGCTCCTG 3660
CysLysArgLysAsnProThrSerCysSerArgArgPheTyrGlnLeuThrLysLeuLeu

GATTCTGTGCAGCCTATTGCAAGAGAGCTGCATCAATTCACCTTTTGACCTGCTAATCAAG 3720
AspSerValGlnProIleAlaArgGluLeuHisGlnPheThrPheAspLeuLeuIleLys

TCCCATATGGTGAGCGTGGACTTTCCTGAAATGATGGCAGAGATCATCTCTGTGCAAGTG 3780
SerHisMetValSerValAspPheProGluMetMetAlaGluIleIleSerValGlnVal

CCCAAGATCCTTTCTGGGAAAGTCAAGCCCATCTATTTCCACACACAGTGAAGATTTGGA 3840
ProLysIleLeuSerGlyLysValLysProIleTyrPheHisThrGlnEnd

ACCTAATACCCAAACCCACCTGTTCCCTTTTCAGATGTCTTCTGCCTGTTATATAACTCT 3900

GCACTACTTCTCTGGCATGGGCCTTGGGGGAAATTCCTCTACTGATGTACAGTCTGTGCAT 3960

GAACATGTTCCCAAGTTCTATTTCTGGGCTTTTCCTTCTTTCTTTTCTTCTTCTCTG 4020

CCTCTTTTACCCTCCCATGGCACATTTTGAATCCGCTGCGTGTTGTGGCTCCTGCCTGTG 4080

TTTTGAGTTTTGTTGTATTTCTTCAAGTCTGTGATGATCTTCTTGTGGCCCAGTGTCAAC 4140

TGTGCTTGTTTATAGCACTGTGCTGTGTGCCAACCAAGCAAATGTTTACTCACCTTATGC 4200

CATGGCAAGTTTAGAGAGCTATAAGTATCTTGGGAAGAAACAAACAGAGAGAGTAAAAAA 4260

ACCAAAAAAAAAAAAAAAAAAACC GAATTC 4289

FIG. 6D